



# 6

SUBSTITUTE SEQUENCE LISTING

<110> RIKEN  
<120> Truncated Reelin Protein and DNA Encoding the Same  
<130> PH-1167  
<140> US 09/832,189  
<141> 2001-04-11  
<150> JP 2000-109954  
<151> 2000-04-11  
<160> 28  
<170> PatentIn Ver. 2.0  
<210> 1  
<211> 2274  
<212> DNA  
<213> Xenopus laevis  
<220>  
<221> misc\_feature  
<222> (100)  
<223> a or g or t or c  
<220>  
<221> CDS  
<222> (157)..(1455)  
<220>  
<221> sig\_peptide  
<222> (157)..(234)  
<220>  
<221> misc\_feature  
<222> (241)..(726)  
<223> F-spondin domain  
<220>  
<221> misc\_feature  
<222> (847)..(1197)  
<223> CR-50 epitope region  
<400> 1  
cattctactg tcacgttaac ttccatttt cttcacttta actttgaaga atttaaaaaa 60  
aaccattaat tatatatatta tataaatata tatatataan ctctgtatcc caggctgctt 120  
atgaagaaag ctcattaaga acagtgggac ccagga atg gaa ctg ctc cac acc 174  
Met Glu Leu Leu His Thr  
1 5  
ttc tgc ggt ggg cgc tgg act ttg ctg ctc ttc acg ggg atc ttg tgc 222  
Phe Cys Gly Gly Arg Trp Thr Leu Leu Phe Thr Gly Ile Leu Cys  
10 15 20  
ttt gtt gtt gcc cgc gga gtg ggg tat tat ccc agg ttc tct cca ttc 270  
Phe Val Val Ala Arg Gly Val Gly Tyr Tyr Pro Arg Phe Ser Pro Phe  
25 30 35

ttt	ttc	ctt	tgc	act	cat	cat	gga	gaa	ctg	gaa	gga	gat	ggg	gaa	caa	318
Phe	Phe	Leu	Cys	Thr	His	His	Gly	Glu	Leu	Glu	Gly	Asp	Gly	Glu	Gln	
	40					45					50					
gga	gaa	gtg	ctc	atc	tct	ctg	cac	ctg	gcg	ggc	aac	ccc	agc	tac	tac	366
Gly	Glu	Val	Leu	Ile	Ser	Leu	His	Leu	Ala	Gly	Asn	Pro	Ser	Tyr	Tyr	
55					60					65					70	
ata	cct	ggg	cag	gag	tac	cat	gtg	acc	ata	tcc	act	agt	acc	ttc	ttt	414
Ile	Pro	Gly	Gln	Glu	Tyr	His	Val	Thr	Ile	Ser	Thr	Ser	Thr	Phe	Phe	
				75					80					85		
gat	ggt	ctt	ctg	gtg	act	gga	ctt	tac	act	tct	acc	agt	gtt	caa	gcg	462
Asp	Gly	Leu	Leu	Val	Thr	Gly	Leu	Tyr	Thr	Ser	Thr	Ser	Val	Gln	Ala	
			90					95					100			
tct	cag	agc	att	gga	ggc	tct	aaa	gca	ttt	gga	ttt	ggt	att	atg	agc	510
Ser	Gln	Ser	Ile	Gly	Gly	Ser	Lys	Ala	Phe	Gly	Phe	Gly	Ile	Met	Ser	
		105					110					115				
gac	cgt	cag	ttt	ggt	acc	cag	ttt	atg	tgc	agt	gtc	ggt	gct	tcc	cac	558
Asp	Arg	Gln	Phe	Gly	Thr	Gln	Phe	Met	Cys	Ser	Val	Val	Ala	Ser	His	
	120					125					130					
gtg	agt	cat	ctt	ccc	aca	aca	aac	cta	agt	ttt	gta	tgg	att	gca	cca	606
Val	Ser	His	Leu	Pro	Thr	Thr	Asn	Leu	Ser	Phe	Val	Trp	Ile	Ala	Pro	
135					140					145					150	
cca	gca	ggt	aca	gga	tgt	gtc	aac	ttc	atg	gcc	aca	gca	aca	cat	agg	654
Pro	Ala	Gly	Thr	Gly	Cys	Val	Asn	Phe	Met	Ala	Thr	Ala	Thr	His	Arg	
				155					160					165		
gga	caa	gtt	att	ttc	aag	gat	gcc	ctg	gca	caa	caa	ctg	tgc	gaa	caa	702
Gly	Gln	Val	Ile	Phe	Lys	Asp	Ala	Leu	Ala	Gln	Gln	Leu	Cys	Glu	Gln	
			170					175					180			
gga	gct	cct	act	gaa	gct	ccc	ttg	cgg	cct	aat	tta	gcc	gaa	att	cac	750
Gly	Ala	Pro	Thr	Glu	Ala	Pro	Leu	Arg	Pro	Asn	Leu	Ala	Glu	Ile	His	
		185					190					195				
agt	gaa	agc	atc	ctt	tta	cga	gat	gat	ttt	gac	tca	tat	aag	ctt	cag	798
Ser	Glu	Ser	Ile	Leu	Leu	Arg	Asp	Asp	Phe	Asp	Ser	Tyr	Lys	Leu	Gln	
	200					205				210						
gaa	ttg	aat	cca	aat	att	tgg	ctc	cag	tgc	aga	aat	tgc	gaa	gtt	ggt	846
Glu	Leu	Asn	Pro	Asn	Ile	Trp	Leu	Gln	Cys	Arg	Asn	Cys	Glu	Val	Gly	
215					220					225					230	
gag	cag	tgt	ggt	gca	att	atg	cat	ggt	ggg	gca	gtc	act	ttt	tgt	gat	894
Glu	Gln	Cys	Gly	Ala	Ile	Met	His	Gly	Gly	Ala	Val	Thr	Phe	Cys	Asp	
				235					240					245		
ccg	tat	gga	cca	aga	gaa	ttg	ata	act	gtt	caa	atg	aac	aca	act	acg	942
Pro	Tyr	Gly	Pro	Arg	Glu	Leu	Ile	Thr	Val	Gln	Met	Asn	Thr	Thr	Thr	
			250					255					260			
gca	tct	gtt	ttg	cag	ttt	tct	att	ggg	tca	gga	tcg	tgc	agg	ttc	agc	990
Ala	Ser	Val	Leu	Gln	Phe	Ser	Ile	Gly	Ser	Gly	Ser	Cys	Arg	Phe	Ser	
		265					270					275				
tat	tca	gac	cct	gga	att	gtg	gtg	tca	tac	aca	aag	aat	aat	tca	tct	1038
Tyr	Ser	Asp	Pro	Gly	Ile	Val	Val	Ser	Tyr	Thr	Lys	Asn	Asn	Ser	Ser	
	280					285					290					

agt tgg atg cca ttg gag aga att agt gct cct tcc aat gtt agc acc 1086  
 Ser Trp Met Pro Leu Glu Arg Ile Ser Ala Pro Ser Asn Val Ser Thr 310  
 295 300 305

atc att cac att att tac cta cct cct gaa gct aaa gga gaa aat gtg 1134  
 Ile Ile His Ile Ile Tyr Leu Pro Pro Glu Ala Lys Gly Glu Asn Val 325  
 315 320

aaa ttc cgt tgg agg cag gag aac atg cag gca ggt gat gtg tat gaa 1182  
 Lys Phe Arg Trp Arg Gln Glu Asn Met Gln Ala Gly Asp Val Tyr Glu 340  
 330 335

gcc tgc tgg gca ctg gat aac att ttg att atc aat gct gct cat aaa 1230  
 Ala Cys Trp Ala Leu Asp Asn Ile Leu Ile Ile Asn Ala Ala His Lys 355  
 345 350

gaa gtc gtg tta gaa gac aat cta gat cca atg gac aca gga aac tgg 1278  
 Glu Val Val Leu Glu Asp Asn Leu Asp Pro Met Asp Thr Gly Asn Trp 370  
 360 365

ctt ttt ttc cct ggg gct act gta aag cat acc tgt cag tcg gat gga 1326  
 Leu Phe Phe Pro Gly Ala Thr Val Lys His Thr Cys Gln Ser Asp Gly 390  
 375 380 385

aac tct ata tat ttt cat ggt aca gaa agc agt gaa tac aac ttt gct 1374  
 Asn Ser Ile Tyr Phe His Gly Thr Glu Ser Ser Glu Tyr Asn Phe Ala 405  
 395 400

act acc aga gat gtg gat ctt tcc agt gag gac atc cag gac cag tgg 1422  
 Thr Thr Arg Asp Val Asp Leu Ser Ser Glu Asp Ile Gln Asp Gln Trp 420  
 410 415

tct gaa gag ttt gag aat cta cca gct ggg taa attttagatg tagccatgag 1475  
 Ser Glu Glu Phe Glu Asn Leu Pro Ala Gly 430  
 425

cattacattt tatcacgtga aaatgcaaga aacagtattt atatacatat tttaaaggctc 1535

aatacagaac cctataaatg gcagggttagg gctaccatgt aaatattttt aatgttcata 1595

atgtcatagg tggttaagtat ttacatagc agttactgat tgattattat tgtttgtcctt 1655

ttaccagtt acagctaaca cacagggcat ttttttccaa tggcaacatc cattttgccg 1715

ctctgagcag aacatttggt tcatttatgg catttgaacc tgtgtctatg agagtgcagc 1775

taaaataaac ttctgggcta tgggtgttac catacaacac tgggtacctca tgacatatga 1835

aaaatatgac tcacattaaa tcagtaagat cagttcaagt atagtacggt gcattaatct 1895

gccaataaac atttagaatt gtattttata ttttatattt aagattagaa ttgactccat 1955

tcttgacct tgcacacat ttgtggctag tttatggggtc aatagacagc catcatacat 2015

tagtcagagt aaatcgagca ttacaaaact caatgagcca tagtgagtgt gacaatcaga 2075

agtgactgtc aagtaaatca accatttgct catacagatg cacatttgaa cagtggattc 2135

ttatccagaa agggccattt ttactatca ctctgggatt taaatgccac ttctaattgg 2195

aacttccagg tcacaaaaat agaatggaca tttaaacatc atggtttctca ttacccttaa 2255

taaaactccg gttttttta 2274

<210> 2  
 <211> 432  
 <212> PRT  
 <213> xenopus laevis

<400> 2  
 Met Glu Leu Leu His Thr Phe Cys Gly Gly Arg Trp Thr Leu Leu Leu  
 1 5 10 15  
 Phe Thr Gly Ile Leu Cys Phe Val Val Ala Arg Gly Val Gly Tyr Tyr  
 20 25 30  
 Pro Arg Phe Ser Pro Phe Phe Phe Leu Cys Thr His His Gly Glu Leu  
 35 40 45  
 Glu Gly Asp Gly Glu Gln Gly Glu Val Leu Ile Ser Leu His Leu Ala  
 50 55 60  
 Gly Asn Pro Ser Tyr Tyr Ile Pro Gly Gln Glu Tyr His Val Thr Ile  
 65 70 75 80  
 Ser Thr Ser Thr Phe Phe Asp Gly Leu Leu Val Thr Gly Leu Tyr Thr  
 85 90 95  
 Ser Thr Ser Val Gln Ala Ser Gln Ser Ile Gly Gly Ser Lys Ala Phe  
 100 105 110  
 Gly Phe Gly Ile Met Ser Asp Arg Gln Phe Gly Thr Gln Phe Met Cys  
 115 120 125  
 Ser Val Val Ala Ser His Val Ser His Leu Pro Thr Thr Asn Leu Ser  
 130 135 140  
 Phe Val Trp Ile Ala Pro Pro Ala Gly Thr Gly Cys Val Asn Phe Met  
 145 150 155 160  
 Ala Thr Ala Thr His Arg Gly Gln Val Ile Phe Lys Asp Ala Leu Ala  
 165 170 175  
 Gln Gln Leu Cys Glu Gln Gly Ala Pro Thr Glu Ala Pro Leu Arg Pro  
 180 185 190  
 Asn Leu Ala Glu Ile His Ser Glu Ser Ile Leu Leu Arg Asp Asp Phe  
 195 200 205  
 Asp Ser Tyr Lys Leu Gln Glu Leu Asn Pro Asn Ile Trp Leu Gln Cys  
 210 215 220  
 Arg Asn Cys Glu Val Gly Glu Gln Cys Gly Ala Ile Met His Gly Gly  
 225 230 235 240  
 Ala Val Thr Phe Cys Asp Pro Tyr Gly Pro Arg Glu Leu Ile Thr Val  
 245 250 255  
 Gln Met Asn Thr Thr Thr Ala Ser Val Leu Gln Phe Ser Ile Gly Ser  
 260 265 270  
 Gly Ser Cys Arg Phe Ser Tyr Ser Asp Pro Gly Ile Val Val Ser Tyr  
 275 280 285  
 Thr Lys Asn Asn Ser Ser Ser Trp Met Pro Leu Glu Arg Ile Ser Ala  
 290 295 300

B1  
 Cont

Pro Ser Asn Val Ser Thr Ile Ile His Ile Ile Tyr Leu Pro Pro Glu  
 305 310 315 320  
 Ala Lys Gly Glu Asn Val Lys Phe Arg Trp Arg Gln Glu Asn Met Gln  
 325 330 335  
 Ala Gly Asp Val Tyr Glu Ala Cys Trp Ala Leu Asp Asn Ile Leu Ile  
 340 345 350  
 Ile Asn Ala Ala His Lys Glu Val Val Leu Glu Asp Asn Leu Asp Pro  
 355 360 365  
 Met Asp Thr Gly Asn Trp Leu Phe Phe Pro Gly Ala Thr Val Lys His  
 370 375 380  
 Thr Cys Gln Ser Asp Gly Asn Ser Ile Tyr Phe His Gly Thr Glu Ser  
 385 390 395 400  
 Ser Glu Tyr Asn Phe Ala Thr Thr Arg Asp Val Asp Leu Ser Ser Glu  
 405 410 415  
 Asp Ile Gln Asp Gln Trp Ser Glu Glu Phe Glu Asn Leu Pro Ala Gly  
 420 425 430

<210> 3  
 <211> 2745  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (283)..(2052)

<220>  
 <221> sig\_peptide  
 <222> (283)..(363)

<220>  
 <221> misc\_feature  
 <222> (284)..(849)  
 <223> F-spondin domain

<220>  
 <221> misc\_feature  
 <222> (970)..(1320)  
 <223> CR-50 epitope region

<400> 3  
 ggggctgcgtgc gtgcacaccg gcggcgggcg cgctcggagg cggacgacgc gctctcggcg 60  
 cccgcggccc cggttcccc cgcgctctcg ctccggcggc ccaaagtaac ttcgggagcc 120  
 tcggtctccc gctaacttcc ccccgcgggc tcggttgccc ggaccgctc ggctcgagcc 180  
 cgccgccggc tcgccttccc cgcacgcggc tcctccgtgc cggtgccctc gaaagtggat 240  
 gagagagcgc gcggggcgcg cggcggcacg gagcgcgggc gc atg gag cgc ggc 294  
 Met Glu Arg Gly  
 1

tgc tgg gcg ccg cgg gct ctc gtc ctg gcc gtg ctg ctg ctg ctg ggc 342  
 Cys Trp Ala Pro Arg Ala Leu Val Leu Ala Val Leu Leu Leu Leu Ala  
 5 10 15 20

B1  
 cont

acg	ctg	agg	gcg	cg	gcg	gcc	acc	ggc	tac	tac	ccg	cg	ttc	tcg	cct	390
Thr	Leu	Arg	Ala	Arg	Ala	Ala	Thr	Gly	Tyr	Tyr	Pro	Arg	Phe	Ser	Pro	
				25					30					35		
ttc	ttt	ttc	ctg	tgc	acc	cac	cac	ggg	gag	ctg	gaa	ggg	gat	ggg	gag	438
Phe	Phe	Phe	Leu	Cys	Thr	His	His	Gly	Glu	Leu	Glu	Gly	Asp	Gly	Glu	
			40					45					50			
cag	ggc	gag	gtg	ctc	att	tcc	ctg	cac	att	gcg	ggc	aac	ccc	acc	tac	486
Gln	Gly	Glu	Val	Leu	Ile	Ser	Leu	His	Ile	Ala	Gly	Asn	Pro	Thr	Tyr	
		55					60					65				
tac	gta	ccg	gga	cag	gaa	tac	cat	gtt	aca	att	tca	aca	agc	acc	ttc	534
Tyr	Val	Pro	Gly	Gln	Glu	Tyr	His	Val	Thr	Ile	Ser	Thr	Ser	Thr	Phe	
	70					75					80					
ttt	gat	ggc	ttg	ctg	gtg	acg	gga	ctc	tat	acc	tcg	aca	agc	atc	cag	582
Phe	Asp	Gly	Leu	Leu	Val	Thr	Gly	Leu	Tyr	Thr	Ser	Thr	Ser	Ile	Gln	
	85				90				95						100	
tct	tct	cag	agc	att	gga	ggc	tcc	agc	gcc	ttt	gga	ttc	ggg	atc	atg	630
Ser	Ser	Gln	Ser	Ile	Gly	Gly	Ser	Ser	Ala	Phe	Gly	Phe	Gly	Ile	Met	
				105					110					115		
tcc	gac	cac	cag	ttt	ggt	aac	cag	ttt	atg	tgc	agt	gtg	gtg	gcc	tct	678
Ser	Asp	His	Gln	Phe	Gly	Asn	Gln	Phe	Met	Cys	Ser	Val	Val	Ala	Ser	
			120				125					130				
cat	gtg	agt	cac	ctg	cct	aca	acc	aac	ctc	agc	ttt	gtc	tg	att	gcc	726
His	Val	Ser	His	Leu	Pro	Thr	Thr	Asn	Leu	Ser	Phe	Val	Trp	Ile	Ala	
		135					140					145				
cca	cca	gct	ggc	aca	ggc	tgt	gtg	aat	ttc	atg	gct	act	gca	aca	cat	774
Pro	Pro	Ala	Gly	Thr	Gly	Cys	Val	Asn	Phe	Met	Ala	Thr	Ala	Thr	His	
	150					155					160					
agg	ggc	cag	gtg	att	ttc	aaa	gac	gca	ctg	gcc	cag	cag	ctg	tgt	gaa	822
Arg	Gly	Gln	Val	Ile	Phe	Lys	Asp	Ala	Leu	Ala	Gln	Gln	Leu	Cys	Glu	
	165				170				175						180	
caa	gga	gct	ccc	aca	gag	gcc	act	gct	tac	tcg	cac	ctt	gct	gaa	ata	870
Gln	Gly	Ala	Pro	Thr	Glu	Ala	Thr	Ala	Tyr	Ser	His	Leu	Ala	Glu	Ile	
				185					190					195		
cac	agt	gac	agt	gtg	atc	cta	cga	gat	gac	ttt	gac	tcc	tac	cag	caa	918
His	Ser	Asp	Ser	Val	Ile	Leu	Arg	Asp	Asp	Phe	Asp	Ser	Tyr	Gln	Gln	
			200					205					210			
ctg	gaa	ttg	aac	ccc	aac	ata	tgg	gtt	gaa	tgc	agc	aac	tgt	gag	atg	966
Leu	Glu	Leu	Asn	Pro	Asn	Ile	Trp	Val	Glu	Cys	Ser	Asn	Cys	Glu	Met	
		215					220					225				
gga	gag	cag	tgt	ggc	acc	atc	atg	cat	ggc	aat	gct	gtc	acc	ttc	tgt	1014
Gly	Glu	Gln	Cys	Gly	Thr	Ile	Met	His	Gly	Asn	Ala	Val	Thr	Phe	Cys	
	230					235					240					
gag	ccg	tac	ggc	cct	cga	gag	ctg	acc	acc	aca	tgc	ctg	aac	aca	aca	1062
Glu	Pro	Tyr	Gly	Pro	Arg	Glu	Leu	Thr	Thr	Thr	Cys	Leu	Asn	Thr	Thr	
	245				250					255					260	
aca	gca	tct	gtc	ctc	cag	ttt	tcc	att	ggg	tca	gga	tca	tgt	cga	ttt	1110
Thr	Ala	Ser	Val	Leu	Gln	Phe	Ser	Ile	Gly	Ser	Gly	Ser	Cys	Arg	Phe	
				265					270					275		

agt	tac	tct	gac	ccc	agc	atc	act	gtg	tca	tac	gcc	aag	aac	aat	acc	1158
Ser	Tyr	Ser	Asp	Pro	Ser	Ile	Thr	Val	Ser	Tyr	Ala	Lys	Asn	Asn	Thr	
			280					285					290			
gct	gat	tgg	att	cag	ctg	gag	aaa	att	aga	gcc	cct	tcc	aat	gtg	agc	1206
Ala	Asp	Trp	Ile	Gln	Leu	Glu	Lys	Ile	Arg	Ala	Pro	Ser	Asn	Val	Ser	
		295					300					305				
aca	gtc	atc	cac	atc	ctg	tac	ctc	ccc	gag	gaa	gcc	aaa	ggg	gag	agc	1254
Thr	Val	Ile	His	Ile	Leu	Tyr	Leu	Pro	Glu	Glu	Ala	Lys	Gly	Glu	Ser	
	310					315					320					
gtg	cag	ttc	cag	tgg	aaa	cag	gac	agc	ctg	cga	gtg	ggt	gag	gtg	tat	1302
Val	Gln	Phe	Gln	Trp	Lys	Gln	Asp	Ser	Leu	Arg	Val	Gly	Glu	Val	Tyr	
325					330					335					340	
gag	gcc	tgc	tgg	gcc	ctg	gat	aac	atc	ctg	gtc	atc	aat	tca	gcc	cac	1350
Glu	Ala	Cys	Trp	Ala	Leu	Asp	Asn	Ile	Leu	Val	Ile	Asn	Ser	Ala	His	
				345					350					355		
aga	gaa	gtc	gtt	ctg	gag	gac	aac	ctc	gac	ccg	gtc	gac	acg	ggc	aac	1398
Arg	Glu	Val	Val	Leu	Glu	Asp	Asn	Leu	Asp	Pro	Val	Asp	Thr	Gly	Asn	
			360					365					370			
tgg	ctc	ttc	ttc	cct	gga	gca	acg	gtc	aag	cat	agc	tgt	cag	tca	gat	1446
Trp	Leu	Phe	Phe	Pro	Gly	Ala	Thr	Val	Lys	His	Ser	Cys	Gln	Ser	Asp	
		375					380					385				
ggg	aac	tcc	att	tat	ttc	cat	gga	aat	gaa	ggc	agc	gag	ttc	aat	ttt	1494
Gly	Asn	Ser	Ile	Tyr	Phe	His	Gly	Asn	Glu	Gly	Ser	Glu	Phe	Asn	Phe	
	390					395					400					
gcc	acc	acc	cgg	gat	gta	gat	ctt	tct	aca	gag	gat	att	caa	gag	cag	1542
Ala	Thr	Thr	Arg	Asp	Val	Asp	Leu	Ser	Thr	Glu	Asp	Ile	Gln	Glu	Gln	
405					410					415					420	
tgg	tca	gaa	gaa	ttt	gag	agc	cag	ccc	aca	gga	tgg	gat	atc	ttg	gga	1590
Trp	Ser	Glu	Glu	Phe	Glu	Ser	Gln	Pro	Thr	Gly	Trp	Asp	Ile	Leu	Gly	
				425					430					435		
gca	gta	gtt	ggt	gca	gac	tgt	gga	acc	gta	gaa	tca	gga	cta	tca	ctg	1638
Ala	Val	Val	Gly	Ala	Asp	Cys	Gly	Thr	Val	Glu	Ser	Gly	Leu	Ser	Leu	
			440				445						450			
gtg	ttc	ctc	aaa	gat	gga	gag	agg	aag	ctt	tgc	acc	ccc	tac	atg	gat	1686
Val	Phe	Leu	Lys	Asp	Gly	Glu	Arg	Lys	Leu	Cys	Thr	Pro	Tyr	Met	Asp	
		455					460					465				
aca	act	ggt	tat	ggc	aac	ctg	agg	ttc	tac	ttc	gtt	atg	gga	gga	atc	1734
Thr	Thr	Gly	Tyr	Gly	Asn	Leu	Arg	Phe	Tyr	Phe	Val	Met	Gly	Gly	Ile	
	470					475					480					
tgt	gac	cct	gga	gtc	tct	cat	gaa	aac	gat	atc	atc	tta	tat	gca	aag	1782
Cys	Asp	Pro	Gly	Val	Ser	His	Glu	Asn	Asp	Ile	Ile	Leu	Tyr	Ala	Lys	
485					490					495					500	
att	gaa	gga	aga	aaa	gaa	cac	att	gca	ctg	gac	act	ctt	acc	tat	tct	1830
Ile	Glu	Gly	Arg	Lys	Glu	His	Ile	Ala	Leu	Asp	Thr	Leu	Thr	Tyr	Ser	
				505					510					515		
tcc	tat	aag	gtt	ccg	tct	ttg	gtt	tct	gtg	gtc	atc	aac	cct	gaa	ctt	1878
Ser	Tyr	Lys	Val	Pro	Ser	Leu	Val	Ser	Val	Val	Ile	Asn	Pro	Glu	Leu	
			520					525					530			

cag aca cct gcc acc aaa ttt tgt ctc agg caa aag agc cac caa ggg 1926  
Gln Thr Pro Ala Thr Lys Phe Cys Leu Arg Gln Lys Ser His Gln Gly  
535 540 545

tat aat cgg aat gtc tgg gct gtg gac ttc ttc cat gtg ctg ccc gtt 1974  
Tyr Asn Arg Asn Val Trp Ala Val Asp Phe Phe His Val Leu Pro Val  
550 555 560

ctc cct tca aca atg tct cac atg atc cag ttt tct att aat ttg gga 2022  
Leu Pro Ser Thr Met Ser His Met Ile Gln Phe Ser Ile Asn Leu Gly  
565 570 575 580

tgc ggc aca cac cag cct ggg aac agg tga gaagcatgcc gagtgtccta 2072  
Cys Gly Thr His Gln Pro Gly Asn Arg  
585

acatggtagg aaataaacac atgcactgga ccattgaagt aagtttgtca gtaggatttt 2132

tggtatgggat tttaacaaaa tatccattaa gaaaatacag attcctactc cctccctaaa 2192

agagttcttt ggtaataaaa tagaagggat gtgactgggt agatttttag gttagaatag 2252

tttcattcag ggagcttgat acaagttatc agagggtgtc accatgctgt gtggcagcat 2312

cccccttct aacagattgc tgggtgaaga tgactgaaga caagattggc ttctgttggc 2372

tggtgacccc ttataatagg tatggaagtc aattagcact tcaagggcta tgacttctct 2432

gctcctcttg cataagtgtt gctcccatcc tctgtaaaga actttgctga cctcacattc 2492

acaggatgaa gtgacagtgt gagacatggt aattgcctag ctatctatca aattcaagag 2552

cacaaacca gtttactgtg tattgtcctt cagacgtagc ttttatggca gtaatccaat 2612

ggcttgccct ctgaaggctg gtcaggcttc agtgagagat gacacattta gtaaaggctt 2672

tagagaaatc ccacattcat cgactcattc aagggtattta gctagaaata aaaagaatca 2732

aaaaaataaa tta 2745

<210> 4  
<211> 589  
<212> PRT  
<213> Mus musculus

<400> 4  
Met Glu Arg Gly Cys Trp Ala Pro Arg Ala Leu Val Leu Ala Val Leu  
1 5 10 15

Leu Leu Leu Ala Thr Leu Arg Ala Arg Ala Ala Thr Gly Tyr Tyr Pro  
20 25 30

Arg Phe Ser Pro Phe Phe Phe Leu Cys Thr His His Gly Glu Leu Glu  
35 40 45

Gly Asp Gly Glu Gln Gly Glu Val Leu Ile Ser Leu His Ile Ala Gly  
50 55 60

Asn Pro Thr Tyr Tyr Val Pro Gly Gln Glu Tyr His Val Thr Ile Ser  
65 70 75 80

Thr Ser Thr Phe Phe Asp Gly Leu Leu Val Thr Gly Leu Tyr Thr Ser

B1  
CMT



85

90

95

Thr Ser Ile Gln Ser Ser Gln Ser Ile Gly Gly Ser Ser Ala Phe Gly  
 100 105 110  
 Phe Gly Ile Met Ser Asp His Gln Phe Gly Asn Gln Phe Met Cys Ser  
 115 120 125  
 Val Val Ala Ser His Val Ser His Leu Pro Thr Thr Asn Leu Ser Phe  
 130 135 140  
 Val Trp Ile Ala Pro Pro Ala Gly Thr Gly Cys Val Asn Phe Met Ala  
 145 150 155 160  
 Thr Ala Thr His Arg Gly Gln Val Ile Phe Lys Asp Ala Leu Ala Gln  
 165 170 175  
 Gln Leu Cys Glu Gln Gly Ala Pro Thr Glu Ala Thr Ala Tyr Ser His  
 180 185 190  
 Leu Ala Glu Ile His Ser Asp Ser Val Ile Leu Arg Asp Asp Phe Asp  
 195 200 205  
 Ser Tyr Gln Gln Leu Glu Leu Asn Pro Asn Ile Trp Val Glu Cys Ser  
 210 215 220  
 Asn Cys Glu Met Gly Glu Gln Cys Gly Thr Ile Met His Gly Asn Ala  
 225 230 235 240  
 Val Thr Phe Cys Glu Pro Tyr Gly Pro Arg Glu Leu Thr Thr Thr Cys  
 245 250 255  
 Leu Asn Thr Thr Thr Ala Ser Val Leu Gln Phe Ser Ile Gly Ser Gly  
 260 265 270  
 Ser Cys Arg Phe Ser Tyr Ser Asp Pro Ser Ile Thr Val Ser Tyr Ala  
 275 280 285  
 Lys Asn Asn Thr Ala Asp Trp Ile Gln Leu Glu Lys Ile Arg Ala Pro  
 290 295 300  
 Ser Asn Val Ser Thr Val Ile His Ile Leu Tyr Leu Pro Glu Glu Ala  
 305 310 315 320  
 Lys Gly Glu Ser Val Gln Phe Gln Trp Lys Gln Asp Ser Leu Arg Val  
 325 330 335  
 Gly Glu Val Tyr Glu Ala Cys Trp Ala Leu Asp Asn Ile Leu Val Ile  
 340 345 350  
 Asn Ser Ala His Arg Glu Val Val Leu Glu Asp Asn Leu Asp Pro Val  
 355 360 365  
 Asp Thr Gly Asn Trp Leu Phe Phe Pro Gly Ala Thr Val Lys His Ser  
 370 375 380  
 Cys Gln Ser Asp Gly Asn Ser Ile Tyr Phe His Gly Asn Glu Gly Ser  
 385 390 395 400  
 Glu Phe Asn Phe Ala Thr Thr Arg Asp Val Asp Leu Ser Thr Glu Asp  
 405 410 415  
 Ile Gln Glu Gln Trp Ser Glu Glu Phe Glu Ser Gln Pro Thr Gly Trp  
 420 425 430

Asp Ile Leu Gly Ala Val Val Gly Ala Asp Cys Gly Thr Val Glu Ser  
 435 440 445  
 Gly Leu Ser Leu Val Phe Leu Lys Asp Gly Glu Arg Lys Leu Cys Thr  
 450 455 460  
 Pro Tyr Met Asp Thr Thr Gly Tyr Gly Asn Leu Arg Phe Tyr Phe Val  
 465 470 475 480  
 Met Gly Gly Ile Cys Asp Pro Gly Val Ser His Glu Asn Asp Ile Ile  
 485 490 495  
 Leu Tyr Ala Lys Ile Glu Gly Arg Lys Glu His Ile Ala Leu Asp Thr  
 500 505 510  
 Leu Thr Tyr Ser Ser Tyr Lys Val Pro Ser Leu Val Ser Val Val Ile  
 515 520 525  
 Asn Pro Glu Leu Gln Thr Pro Ala Thr Lys Phe Cys Leu Arg Gln Lys  
 530 535 540  
 Ser His Gln Gly Tyr Asn Arg Asn Val Trp Ala Val Asp Phe Phe His  
 545 550 555 560  
 Val Leu Pro Val Leu Pro Ser Thr Met Ser His Met Ile Gln Phe Ser  
 565 570 575  
 Ile Asn Leu Gly Cys Gly Thr His Gln Pro Gly Asn Arg  
 580 585

<210> 5  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:synthetic DNA

<220>  
 <221> modified\_base  
 <222> (8)  
 <223> i

<400> 5  
 arttyggnaa ycarttyatg tg

22

<210> 6  
 <211> 16  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:synthetic DNA

<400> 6  
 tgytccccat ycartt

16

<210> 7  
 <211> 20  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 7

atgtcctcac tggaaagatc

20

<210> 8

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 8

cagcaacaca taggggacaa

20

<210> 9

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 9

ggccacgcgt cgactagtac gaattcatct atagcttttt tttttttttt t

51

<210> 10

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 10

cagtgtcggt gcttcccacg tgagtcacat tcca

35

<210> 11

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 11

cgacaggtac aggatgtgtc aacttcatgg ccaca

35

<210> 12

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

B1  
Cont

<400> 12  
tcccacaaca aacctaagtt 20

<210> 13  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic DNA

<400> 13  
atgtcctcac tggaaagatc 20

<210> 14  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic DNA

<400> 14  
cgggataaca ttcagggtat cact 24

<210> 15  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic DNA

<400> 15  
atccatggcg gtaactgtct tcct 24

<210> 16  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic DNA

<400> 16  
gtcctgatct acaaacacct gctact 26

<210> 17  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic DNA

<400> 17  
aggtagcaca tggacaaaat cc 22

<210> 18  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic DNA

<400> 18  
ctgaagcaaa ccagtcaccg tgggtca

26

<210> 19  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic DNA

<400> 19  
tagtgagtgt gacaatcaga agtga

25

<210> 20  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic DNA

<400> 20  
ggccctttct ggataagaat c

21

<210> 21  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic DNA

<400> 21  
tcaaccattt gtcatacag atgcaca

27

<210> 22  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic DNA

<400> 22  
cctccaagtc tgcctttatg

20

<210> 23  
<211> 20  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 23

gcggacaaca atatgcaagg

20

<210> 24

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 24

gcggacaaca atatgcaagg

20

<210> 25

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 25

ggttggtgac aaactggtcc

20

<210> 26

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 26

cgcgtcgact agtacgaatt

20

<210> 27

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 27

ctgattggat tcagctggag

20

<210> 28

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

B1  
cont

B'

<400> 28  
attcagccca cagagaagtc

20

---